


```
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ039025; AAK82649.1; -.
DR HSSP; P01869; IAE6.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 65.4%; Score 390.5; DB 2; Length 159;
Best Local Similarity 60.0%; Pred. No. 3,1e-33;
Matches 78; Conservative 16; Mismatches 19; Indels 17; Gaps 2;

QY 1 VOLLESGAEVKKRPGASVTITSCQASRODPFGQYIHVVRQAPGCGFEMMGIIINSGGSANY 60
DB 21 VOLV-OSGAEVKKRPGASVSKASGYTFSNYYMMVRQAPGCGPEMMGVINPSGGSARY 79
QY 61 APFKGRLTMSRDSSTDTVYMTLTSLEDTAVYVYCCLO-----ALKHW 104
DB 80 AQKFGQRYMTTRDTSTSTVYMTLSLSKSDDTAVYFCAREMEITFGCAVSKGYFYGGMDV 139
QY 105 GQGTLVAVSS 114
DB 140 GQGTVTVSS 149

RESULT 3
HVLB HUMAN STANDARD; PRT; 117 AA.
ID P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V-I region Hg3 precursor.
OS Homo sapiens (human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakur R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
(VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUG.
DR HSSP; P01751; INQB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1PE7 CRC64;

Query Match 63.2%; Score 376.5; DB 1; Length 117;
Best Local Similarity 74.0%; Pred. No. 6.6e-32;
Matches 71; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 VOLLESGAEVKKRPGASVTITSCQASRODPFGQYIHVVRQAPGCGFEMMGIIINSGGSANY 60
DB 21 VOLV-OSGAEVKKRPGASVSKASGYTFSNYYMMVRQAPGCGLEMMGVINPSGGSARY 79
QY 61 APFKGRLTMSRDSSTDTVYMTLTSLEDTAVYVYCC 96
DB 80 AQKFGQRYMTTRDTSTSTVYMTLSLSRSDTAVYVYCC 115

RESULT 4
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95;
AC Q9UL95;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment) .
OS Homo sapiens (human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998) .
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488BAC CRC64;

Query Match 62.4%; Score 372; DB 2; Length 125;
Best Local Similarity 58.4%; Pred. No. 2,1e-31;
Matches 73; Conservative 15; Mismatches 25; Indels 12; Gaps 2;

QY 1 VOLLESGAEVKKRPGASVTITSCQASRODPFGQYIHVVRQAPGCGFEMMGIIINSGGSANY 60
DB 2 VOLV-OSGAEVKKRPGASVSKASGYTFGYMMHVRQAPGCGLEMMGVINPSGGSARY 60
QY 61 APFKGRLTMSRDSSTDTVYMTLTSLEDTAVYVYCC-----QALGHMGQGT 109
DB 61 AQKFGQRYMTTRDTSTSTVYMTLSLSRSDTAVYVYCARSGGRIAAAGDAPFIWQGT 120
QY 110 VAVSS 114
DB 121 VTVSS 125

RESULT 5
Q6N095 PRELIMINARY; PRT; 475 AA.
ID Q6N095
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AC O6N095;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686K03196.
 GN Name=DKFZp686K03196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Mambout R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Fodo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640621; CAE45775.1; -
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein_1
 SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

Query Match 62.0%; Score 369.5; DB 2; Length 475;
 Best Local Similarity 61.1%; Pred. No. 1.8e-30;
 Matches 77; Conservative 10; Mismatches 26; Indels 13; Gaps 2;

OY 1 VOLLESGAEVKKRPGASVTISCOASRODFSGQYIHWVROAPGCGFEMWGIINPSSGSANY 60
 DB 21 VOLV--SGAEVKKRPGASVTISCRASGYSFSTYHWHVROAPGQLEWGMGINPSSDKTY 79
 OY 61 APKFKRLTMSRSDSTDTVYMTLTSLTSEPTAVYCYL-----LQALKMGCGT 108
 DB 80 AQKFGKVTMTKDTSTSTVFMELNSLMSGDTAVYCTRRDSGRALMGELDAPIMQGT 139
 OY 109 LVAVSS 114
 DB 140 KTVSS 145
 RESULT 6
 Q9UL94 PRELIMINARY; PRT; 119 AA.
 ID Q9UL94;
 AC Q9UL94;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035020; AAD56256.1; -
 DR HSSP; P01751; INQB.

DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345FA16E CRC64;
 Query Match 61.9%; Score 369; DB 2; Length 119;
 Best Local Similarity 60.5%; Pred. No. 4.2e-31;
 Matches 72; Conservative 16; Mismatches 25; Indels 6; Gaps 2;

OY 1 VOLLESGAEVKKRPGASVTISCOASRODFSGQYIHWVROAPGCGFEMWGIINPSSGSANY 60
 DB 2 VOLV--SGAEVKKRPGASVTKVSCASGYTFGTGYVWHVROAPGQLEWGMGINPSSWTNY 60
 OY 61 APKFKRLTMSRSDSTDTVYMTLTSLTSEPTAVYCYLQ-----LKGWCGTLLVAVSS 114
 DB 61 AQKFGKVTMTKDTSTSTVFMELNSLMSGDTAVYCTRRDSGRALMGELDAPIMQGT 119

RESULT 7
 Q6N041 PRELIMINARY; PRT; 498 AA.
 ID Q6N041;
 AC Q6N041;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686O16217 (Fragment).
 GN Name=DKFZp686O16217;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Oeanger A., Fodo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640710; CAE45829.1; -
 DR HSSP; P01751; IAGW.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein_1
 FT NON_TER 1
 SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 61.2%; Score 364.5; DB 2; Length 498;
 Best Local Similarity 56.5%; Pred. No. 6.5e-30;
 Matches 70; Conservative 20; Mismatches 23; Indels 11; Gaps 2;
 OY 1 VOLLESGAEVKKRPGASVTISCOASRODFSGQYIHWVROAPGCGFEMWGIINPSSGSANY 60
 DB 36 VOLV--SGADVKKRPGASVTKVSCASGYTFNFFVWHVROAPGQLEWGMGINPSSDKTY 94
 OY 61 APKFKRLTMSRSDSTDTVYMTLTSLTSEPTAVYCYLQ-----LKGWCGTLLV 110
 DB 95 AQKFGKVTMTKDTSTSTVFMELNSLMSGDTAVYCTRRDSGRALMGELDAPIMQGT 154
 OY 111 AVSS 114
 DB 155 TVSS 158

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RESULT 8
HVIC_HUMAN STANDARD; PRT; 147 AA.
ID HVIC_HUMAN P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
CC protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01751; INOB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006953; P:immune response; NAS.
DR InterPro: IPR007110; Ig_V.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region;
KW Pyridolone carboxylic acid; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 Ig heavy chain V-I region ND.
FT DOMAIN 20 131 Ig-like.
FT MOD_RES 20 20 Pyridolone carboxylic acid.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (in Ref. 2).
FT CONFLICT 53 54 IH -> HI (in Ref. 2).
FT CONFLICT 67 68 IG -> GV (in Ref. 2).
FT CONFLICT 125 125 Missing (in Ref. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948FPF7A25366C0 CRC64;

Query Match 59.7%; Score 356; DB 1; Length 147;
Best Local Similarity 54.4%; Pred. No. 1.3e-29;
Matches 68; Conservative 15; Mismatches 28; Indels 14; Gaps 1;
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AC 065ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
RL EMBL; Y13057; CAA73500.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PR00447; IGV; 2.
DR SMART: SM00409; IGV; 2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F7868338F2BF CRC64;

Query Match 59.1%; Score 352; DB 2; Length 244;
Best Local Similarity 56.2%; Pred. No. 6e-29;
Matches 68; Conservative 18; Mismatches 27; Indels 8; Gaps 2;

QY 1 VOLDSGAEVRRPGASVYITSCQASRODPFGQYIHVWRQAPGGFEMMGITNSGGSANY 60
DB 2 VOLV-OSGAEVRRPGASVYITSCQASGYTSDHYHWRQAPGGFEMMGITNSGDTNR 60
QY 61 ARFKRLTMSRDSSTDTVYMTLSLTSEDTAVVYC-----LQALKHMGGTLVAVS 113
DB 61 AGRFGRVMTSDTSTSAVMEVSRISRDPTAVVYCARGTGSAITGMVDVGGTLVTVS 120
QY 114 S 114
DB 121 S 121

RESULT 10
Q6N030 PRELIMINARY; PRT; 518 AA.
ID Q6N030;
AC 06N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686115212.
GN Name=DKFZp686115212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RA The German Human cDNA Consortium;
RA Pouskka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amlid C., Oeinger A., Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBD databases.
DR EMBL; BX640724; CAA45841.1; -.
DR HSSP; P01861; IADQ.
DR InterPro: IPR000005; HTNARC.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
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DR Pfam: PF07654; Cl-sect: 3.
DR SMART: SM00409; IG: 3.
DR SMART: SM00407; IGL: 3.
DR SMART: SMD0406; IGv: 1.
DR PROSITE: PS00041; HTM ARAC FAMILY_1; UNKNOWN_1.
DR PROSITE: PSS0835; IG_Like: 4.
DR PROSITE: PSS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match      58.4%; Score 348; DB 2; Length 518;
Best Local Similarity 57.1%; Pred. No. 3,8e-28;
Matches 68; Conservative 15; Mismatches 28; Indels 8; Gaps 1.

OY 4 LEQSGAEVKRPGASVTTISCOASRDPSGQYIHWVAQPAGQGFEMNGIINPSCGSANYAPK 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
DB 23 LVQSGAEVKKPGASVKVSCTAASGYFTFHFIWMVAQAPQSLEWGMVINTGNKTYSQK 82
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
OY 64 FKGRITMRDSDTDVVMVTLSLTSEDPNAVYYCLLQ-----LKRMGGTLYAVSS 114
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
DB 83 FQGRVTLTRDTWTMTTAAYMDLSLRSEDPAVYWCAADPAQGVTTYTFDYWGQTIVTVSS 141
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |

RESULT 11
O9GWZ2 PRELIMINARY; PRT; 119 AA.
ID O9GWZ2
AC O9GWZ2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OC Schistosoma japonicum (Blood fluke).
CC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
CX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.O., Guan X.H.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF282622; AAC01452.1; -.
DR HSRP; P01751; 1A6W.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match      58.2%; Score 347; DB 2; Length 119;
Best Local Similarity 58.8%; Pred. No. 8,9e-29;
Matches 70; Conservative 13; Mismatches 30; Indels 6; Gaps 2;

OY 1 VOLLEQSGAEVKRPGASVTTISCOASRDPSGQYIHWVAQPAGQGFEMNGIINPSCGSANY 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
DB 2 VOLVE-SGAEVKRKPGASVRVSCAKSAGYFTFGYMMWVAQAGHGHEWIGVINPRGYINY 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
OY 61 APKRGRLTMRDSDTDVVMVTLSLTSEDPNAVYYCLL----QALKRMGGTLYAVSS 114
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
DB 61 NQFKDRVLTMTTKDSFSSTAAMDLSLRSDADSAVYYCARYDDHYCLDWGGQITVTVSS 119
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |

RESULT 12
O8WY24 PRELIMINARY; PRT; 497 AA.
ID O8WY24
AC O8WY24;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE SNG66 protein.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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| Query Match | Best Local Similarity | Score | DB 2 | Length | 497 |
|-------------|--|--------------|--------------|------------------|-------------|
| Matches | 67 | Conservative | 17 | Mismatches | 27 |
| | | | | Indels | 11 |
| | | | | Gaps | 1 |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homimidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| ON | (1) | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong O. | | | | |
| RL | Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases. | | | | |
| DR | EMBL; AF283666; AAL36987.1; -- | | | | |
| DR | HSSP; P01876; IOM0. | | | | |
| DR | Pfam; PF07654; Cl-sect. 2. | | | | |
| DR | SMART; SM00406; IGV. 1. | | | | |
| DR | PROSITE; PS00835; IG_LIKE; 4. | | | | |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN. 1. | | | | |
| SO | SEQUENCE | 497 AA; | 53665 MW; | F24D08DFA5A663E5 | CRC64; |
| Query Match | Best Local Similarity | 57.3%; | Score 341.5; | DB 2; | Length 497; |
| Matches | 67 | Conservative | 17 | Mismatches | 27 |
| | | | | Indels | 11 |
| | | | | Gaps | 1 |
| OY | 4 LEQSGAEYKRPQASVTTCQASRODPSGOYIHWYRAQPGQFEMNGIINPSGGSANYAPK | 63 | | | |
| DB | 23 LEQSGAEYTKPGASVYKSCKASGYFFIYVDINWYQAPQGGLEWGMNMPQTGNTEFAOK | 82 | | | |
| OY | 64 FKGRLTNRSDSTDPVYVMTLTSLTSEDPNAVYYCLLQAK-----HHGQGLVAV | 112 | | | |
| DB | 83 FQGRLTFRSDTSINTAYVLTSLTSDSALYFCARGNLGGRGFGYNNFDPWGHGTLTV | 142 | | | |
| OY | 113 SS 114 | | | | |
| DB | 143 SS 144 | | | | |
| RESULT 13 | | | | | |
| ID | O924Q1 | PRELIMINARY; | PRT; | 142 AA. | |
| AC | O924Q1. | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | | |
| DE | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) | | | | |
| DE | V23-D-J-C mu protein (Fragment). | | | | |
| GN | Name=V23-D-J-C mu; | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | (1) | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C57BL/6; | | | | |
| RA | Kozono Y., Kozono H., Azuma T.; | | | | |
| RL | Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases. | | | | |
| DR | EMBL; AB065913; BAB3929.1; -- | | | | |
| DR | PIR; F33932; F33932. | | | | |
| DR | PIR; I28833; I28833. | | | | |
| DR | PIR; PH0985; PH0985. | | | | |
| DR | PIR; PH1155; PH1155. | | | | |
| DR | PIR; PH1156; PH1156. | | | | |
| DR | PIR; PH1157; PH1157. | | | | |
| DR | PIR; PH1158; PH1158. | | | | |
| DR | HSSP; P01751; IAGW. | | | | |
| DR | SMART; SM00406; IGV. 1. | | | | |
| DR | PROSITE; PS50835; IG_LIKE; 1. | | | | |
| FT | NON TER | 1 | | | |
| FT | NON TER | 1 | | | |
| FT | NON TER | 1 | | | |
| SO | SEQUENCE | 142 AA; | 15622 MW; | 24A265CE4EA318B | CRC64; |
| Query Match | Best Local Similarity | 57.1%; | Score 340.5; | DB 2; | Length 142; |
| Matches | 63 | Conservative | 19 | Mismatches | 29 |
| | | | | Indels | 3 |
| | | | | Gaps | 1 |
| OY | 4 LEQSGAEYKRPQASVTTCQASRODPSGOYIHWYRAQPGQFEMNGIINPSGGSANYAPK | 63 | | | |
| DB | 4 LQDPGTLYVKGASVYKSCKASGYTFTSYMMHWKORPGGLEWIGNINPSNGGTINKEK | 63 | | | |
| OY | 64 FKGRLTNRSDSTDPVYVMTLTSLTSEDPNAVYYCL---LQALKHNGQGLTVAVSS | 114 | | | |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 05:52:18 ; Search time 39 Seconds

(Without alignments)
281.249 Million cell updates/sec

Title: US-09-936-964A-36

Perfect score: 596
Sequence: 1 VQLLESGSGAEVRRPGASVTI.....YCLLQALKHMGQGLVAVSS 114Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 418 | 70.1 | 142 | 2 A32483 | Ig heavy chain V r |
| 2 | 398.5 | 66.9 | 118 | 2 S36265 | Ig heavy chain V r |
| 3 | 391 | 65.6 | 121 | 2 S20783 | Ig heavy chain V r |
| 4 | 388.5 | 65.2 | 135 | 2 S49530 | anti-Sm antibody V |
| 5 | 385 | 64.6 | 123 | 2 D33548 | Ig heavy chain V-1 |
| 6 | 376.5 | 63.2 | 98 | 2 S26520 | Ig heavy chain V r |
| 7 | 376.5 | 63.2 | 117 | 1 HVH0HG | Ig heavy chain V r |
| 8 | 374 | 62.8 | 126 | 2 I44151 | Ig heavy chain V r |
| 9 | 366.5 | 61.5 | 137 | 2 C41287 | Ig heavy chain pre |
| 10 | 365 | 61.2 | 129 | 2 S46393 | Ig heavy chain V r |
| 11 | 362 | 60.7 | 110 | 2 PH1669 | Ig heavy chain V r |
| 12 | 361.5 | 60.7 | 109 | 2 PH1668 | Ig heavy chain V r |
| 13 | 358.5 | 60.2 | 171 | 2 S23623 | Ig heavy chain V r |
| 14 | 358 | 60.1 | 129 | 2 A33548 | Ig heavy chain V-1 |
| 15 | 356.5 | 59.8 | 120 | 2 PH0962 | Ig heavy chain V r |
| 16 | 356 | 59.7 | 143 | 1 E1HUND | Ig heavy chain pre |
| 17 | 355.5 | 59.6 | 120 | 2 S31999 | Ig heavy chain V r |
| 18 | 354 | 59.4 | 125 | 2 PH0957 | Ig heavy chain V r |
| 19 | 353.5 | 59.3 | 136 | 2 S31600 | Ig heavy chain V r |
| 20 | 352.5 | 59.1 | 116 | 2 PH0959 | Ig heavy chain V r |
| 21 | 351 | 58.9 | 127 | 2 S34014 | Ig heavy chain V r |
| 22 | 350.5 | 58.8 | 128 | 2 PH0952 | Ig heavy chain V r |
| 23 | 350 | 58.7 | 119 | 2 PH0961 | Ig heavy chain V r |
| 24 | 349.5 | 58.6 | 98 | 2 S26338 | Ig heavy chain V r |
| 25 | 349.5 | 58.6 | 117 | 2 S18551 | Ig heavy chain V r |
| 26 | 349.5 | 58.6 | 125 | 2 S68170 | Ig heavy chain V r |
| 27 | 348.5 | 58.5 | 122 | 2 PH0958 | Ig heavy chain V r |
| 28 | 348.5 | 58.5 | 136 | 2 PH0536 | Ig heavy chain V r |
| 29 | 347.5 | 58.3 | 104 | 2 S69899 | Ig heavy chain V r |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 347 | 58.2 | 127 | 2 PH0955 | Ig heavy chain V r |
| 31 | 344.5 | 57.8 | 126 | 2 B33548 | Ig heavy chain V-1 |
| 32 | 344.5 | 57.8 | 132 | 2 PH0954 | Ig heavy chain V r |
| 33 | 344 | 57.7 | 108 | 2 PH1664 | Ig heavy chain V r |
| 34 | 343 | 57.6 | 133 | 2 C33548 | Ig heavy chain V-1 |
| 35 | 343 | 57.6 | 135 | 2 PH0953 | Ig heavy chain V r |
| 36 | 343 | 57.6 | 627 | 2 S14683 | Ig mu chain precu |
| 37 | 342.5 | 57.5 | 122 | 2 C49590 | Ig heavy chain V r |
| 38 | 341.5 | 57.3 | 98 | 2 S26912 | Ig heavy chain V r |
| 39 | 341.5 | 57.3 | 136 | 2 PH0960 | Ig heavy chain V r |
| 40 | 340.5 | 57.1 | 119 | 2 D30562 | Ig heavy chain V r |
| 41 | 340.5 | 57.1 | 132 | 2 S31596 | Ig heavy chain V r |
| 42 | 340 | 57.0 | 104 | 2 PH1665 | Ig heavy chain V r |
| 43 | 339.5 | 57.0 | 116 | 2 S55542 | Ig heavy chain V r |
| 44 | 339.5 | 57.0 | 117 | 1 HVH035 | Ig heavy chain pre |
| 45 | 339.5 | 57.0 | 117 | 2 S31680 | Ig heavy chain V r |

ALIGNMENTS

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RESULT 1
A32483
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C/Accession: A32483
R/Larick, J.W.; Danielson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borreback, C
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A/Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
A/Reference number: A32483; MUID:89273586; PMID:2499327
A/Accession: A32483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-142 <LAR>
A:Cross-references: GB:M26463
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterocretamer; immunoglobulin
F:25-108/Domain: immunoglobulin homology <IMM>

Query Match          70.1%; Score 418; DB 2; Length 142;
Best Local Similarity 63.8%; Pred. No. 6; Se-32;
Matches 81; Conservative 15; Mismatches 17; Indels 14; Gaps 2;

QY      1 VQLLESGAEVRRPGASVTISCQASRDPSGGYIHVWRQAPQGFEMNGIINPSGGSANY 60
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Db      12 VQLV-QSGAEVKKPGASVVKSCASGYPTNTYMHVWRQAPQGLEWMGIINPSGNSY 70

QY      61 ARKFKGRLLMSRDSSTDTYYMLTSLTSEDTAVYIC-----LLOALKHMGCG 107
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      71 ACKFGQRYVTRDSTSTVYMLSLRSDSDAVYVCAREKLAATTIFGVLIINGMDYWGCG 130

QY      108 TLAVVSS 114
      ||| |||
Db      131 TLTVVSS 137

RESULT 2
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C/Accession: S36265
R/Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36265; MUID:93178448; PMID:7679990
A/Accession: S36265
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-118 <GRI>
A:Cross-references: EMBL:218846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C/Superfamily: immunoglobulin V region; immunoglobulin homology
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Db 121 QGTLVTSS 129

RESULT 15

PH0962
Ig heavy chain V region (G6+ T-L42) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0962
R:Martin, T.; Dufly, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0962
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-120 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-108/Region: complementarity-determining 3

Query Match 59.8%; Score 356.5; DB 2; Length 120;
Best Local Similarity 61.7%; Pred. No. 2.8e-26;
Matches 74; Conservative 13; Mismatches 26; Indels 7; Gaps 2;

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| | | : : : : : : : : : | |
| Db | 2 | VQLV-QSGAEVKKKPGSSVKVCKASGGTFSYVAISWVROAPGQGLEWMGGIIPFGTANY | 60 |
| | | : : : : : : : : | |
| QY | 61 | APKFKGLTMSRDSSTDTVVTLTSLTSEPTAVVYCLLQAL-----KHNGQGLVAVSS | 114 |
| | | : : : : : : : : | |
| Db | 61 | AKFKGAVTTADBSTSTAIWELSSLRSEDTAVVYCARGVAGRPHPDYMGGTLVTSS | 120 |
| | | : : : : : : : : | |

Search completed: November 9, 2005, 05:59:53
Job time : 40 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model1

Run on: November 9, 2005, 05:52:18 ; Search time 22 Seconds

(without alignments)
386.818 Million cell updates/sec

Title: US-09-936-964A-36

Perfect score: 596
Sequence: 1 VQLLEQSGAVKRGASVTI.....YCLLQALKHGWGQETLVAVSS 114

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCITUS.COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 396.5 | 66.5 | 120 | 3 | US-09-025-769B-36 |
| 2 | 396.5 | 66.5 | 120 | 3 | US-09-025-769B-59 |
| 3 | 396.5 | 66.5 | 120 | 4 | US-09-480-070A-36 |
| 4 | 396.5 | 66.5 | 120 | 4 | US-09-480-070A-59 |
| 5 | 396.5 | 66.5 | 120 | 4 | US-09-490-153-36 |
| 6 | 396.5 | 66.5 | 120 | 4 | US-09-490-153-59 |
| 7 | 396.5 | 66.5 | 120 | 4 | US-09-490-324-36 |
| 8 | 396.5 | 66.5 | 120 | 4 | US-09-490-324-59 |
| 9 | 391 | 65.6 | 123 | 1 | US-08-477-877B-94 |
| 10 | 391 | 65.6 | 123 | 2 | US-08-472-281A-94 |
| 11 | 391 | 65.6 | 123 | 2 | US-08-477-989B-94 |
| 12 | 389 | 65.3 | 117 | 3 | US-09-025-769B-22 |
| 13 | 389 | 65.3 | 117 | 4 | US-09-490-070A-22 |
| 14 | 389 | 65.3 | 117 | 4 | US-09-490-153-22 |
| 15 | 389 | 65.3 | 117 | 4 | US-09-480-324-22 |
| 16 | 380 | 63.8 | 470 | 4 | US-09-859-053-28 |
| 17 | 376.5 | 63.2 | 97 | 2 | US-08-290-592B-16 |
| 18 | 376.5 | 63.2 | 97 | 5 | PCT-US96-09448-16 |
| 19 | 376.5 | 63.2 | 117 | 3 | US-08-545-809A-128 |
| 20 | 373.5 | 62.7 | 116 | 2 | US-08-561-521-41 |
| 21 | 373.5 | 62.7 | 116 | 5 | PCT-US95-01219-41 |
| 22 | 373.5 | 62.7 | 135 | 1 | US-08-137-117D-102 |
| 23 | 373.5 | 62.7 | 135 | 2 | US-08-436-717-102 |
| 24 | 373 | 62.6 | 121 | 4 | US-09-254-180C-7 |
| 25 | 369 | 61.9 | 119 | 4 | US-07-946-421-28 |
| 26 | 369 | 61.9 | 119 | 4 | US-09-438-954-4 |
| 27 | 368.5 | 61.8 | 97 | 5 | PCT-US95-10053-13 |

| | | | | | | |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 368.5 | 61.8 | 135 | 1 | US-08-137-117D-100 | Sequence 100, App |
| 29 | 368.5 | 61.8 | 135 | 2 | US-08-436-717-100 | Sequence 100, App |
| 30 | 368 | 61.7 | 140 | 3 | US-08-836-561-63 | Sequence 63, Appl |
| 31 | 368 | 61.7 | 140 | 4 | US-09-434-122-63 | Sequence 63, Appl |
| 32 | 367.5 | 61.7 | 133 | 3 | US-08-718-323A-8 | Sequence 8, Appl |
| 33 | 367.5 | 61.7 | 133 | 4 | US-09-587-526-8 | Sequence 8, Appl |
| 34 | 366.5 | 61.5 | 118 | 1 | US-08-491-845-14 | Sequence 14, Appl |
| 35 | 366.5 | 61.5 | 137 | 3 | US-08-513-968-38 | Sequence 38, Appl |
| 36 | 364.5 | 61.2 | 120 | 3 | US-09-025-769B-35 | Sequence 35, Appl |
| 37 | 364.5 | 61.2 | 120 | 3 | US-09-025-769B-57 | Sequence 57, Appl |
| 38 | 364.5 | 61.2 | 120 | 4 | US-09-490-070A-35 | Sequence 35, Appl |
| 39 | 364.5 | 61.2 | 120 | 4 | US-09-490-070A-57 | Sequence 57, Appl |
| 40 | 364.5 | 61.2 | 120 | 4 | US-09-490-153-35 | Sequence 35, Appl |
| 41 | 364.5 | 61.2 | 120 | 4 | US-09-490-153-57 | Sequence 57, Appl |
| 42 | 364.5 | 61.2 | 120 | 4 | US-09-490-324-35 | Sequence 35, Appl |
| 43 | 364.5 | 61.2 | 120 | 4 | US-09-490-324-57 | Sequence 57, Appl |
| 44 | 363 | 60.9 | 123 | 2 | US-08-561-521-11 | Sequence 11, Appl |
| 45 | 363 | 60.9 | 123 | 5 | PCT-US95-01219-11 | Sequence 11, Appl |

ALIGNMENTS

RESULT 1
US-09-025-769B-36
Sequence 36, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Knappik, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Mooney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-8090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36
Query Match 66.5%; Score 396.5; DB 3; Length 120;
Best local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;


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      White & McAuliffe
      STREET: 1666 K Street, N.W., Suite 300
      CITY: Washington
      STATE: D.C.
      COUNTRY: USA
      ZIP: 20006
      COMPUTER READABLE FORM:
      MEDIUM TYPE: floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/490,070A
      FILING DATE: 24-Jan-2000
      PRIORITY APPLICATION DATA:
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: Colin G. Sandercock, Esq.
      REGISTRATION NUMBER: 31,298
      REFERENCE/DOCKET NUMBER: 37629-0005
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (202) 912-2000
      TELEFAX: (202) 912-2020
      INFORMATION FOR SEQ ID NO: 59:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 120 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-070A-59

Query Match      66.5%; Score 396.5; DB 4; Length 120;
Best Local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;

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      2 VOLV-QSGAEVYKRGASVYKSCASGYTFISYMHVYRQAPGQGLEWMIINPSGGSANY 60
      61 APKFKGLTMSRDSSTDTVYMTLTSLTSEDTAVYYCL-----LQALKHMGQGLTVAVSS 114
      61 AQKFGQVYMTTRDTISITAYMELSLRSEDTAVYYCARWGSDGFYANDYMGQGLTVAVSS 120
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RESULT 5
US-09-490-153-36
Sequence 36, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
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      FILING DATE: 24-Jan-2000
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/025,769B
      FILING DATE: 18-FEB-1998
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: James F. Haley, Jr., Esq.
      REGISTRATION NUMBER: 27,794
      REFERENCE/DOCKET NUMBER: MORPHO/5
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 596-9000
      TELEFAX: (212) 596-9090
      INFORMATION FOR SEQ ID NO: 36:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 120 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-153-36

Query Match      66.5%; Score 396.5; DB 4; Length 120;
Best Local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;

QY      1 VOLLEQSGAEVYKRGASVITISCOASRODFSGQYIHWYRQAPGQGFEMWGIINSGGSANY 60
      2 VOLV-QSGAEVYKRGASVYKSCASGYTFISYMHVYRQAPGQGLEWMIINPSGGSANY 60
      61 APKFKGLTMSRDSSTDTVYMTLTSLTSEDTAVYYCL-----LQALKHMGQGLTVAVSS 114
      61 AQKFGQVYMTTRDTISITAYMELSLRSEDTAVYYCARWGSDGFYANDYMGQGLTVAVSS 120
      Db

RESULT 6
US-09-490-153-59
Sequence 59, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
```

```

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (212)596-9000
3 TELEFAX: (212)596-9090
4 INFORMATION FOR SEQ ID NO: 59:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 120 amino acids
7 TYPE: amino acid
8 TOPOLOGY: linear
9 MOLECULE TYPE: protein
10 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
11 US-09-490-153-59
12
13 Query Match 66.5%; Score 396.5; DB 4; Length 120;
14 Best Local Similarity 64.2%; Pred. No. 1.8e-33;
15 Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;
16
17 Oy 1 VOLLEQSAEYKRPASVYISQASARQPSGCIYHWRQAPQCGEEMNGIINPSGGSANY 60
18 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
19 Db 2 VOLV-QSAEAYKKPPASVSKASCKAGYFTSTYHMYWQAPQGLMMGMWIPNSGGINY 60
20 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
21 Oy 61 APKFKGRITMSRDSSTDTVYMTLTSLTSEDPYAVYCL-----LQALKHWGGTLVAVSS 114
22 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
23 Db 61 AQKFGGRITMTRDTSISTAYMELSLRREDTAVYVCAMWGQDGFANMYWGGLVTYVSS 120
24 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
25
26 RESULT 7
27 US-09-490-324-36
28 ; Sequence 36, Application US/09490324
29 ; Patent No. 6828422
30 ; GENERAL INFORMATION:
31 APPLICANT: Knappik, Achim
32 Pack, Peter
33 Ilag, Vic
34 Ge, Liming
35 Moroney, Simon
36 Plueckthun, Andreas
37
38 TITLE OF INVENTION: Protein/(poly)peptide libraries
39 NUMBER OF SEQUENCES: 373
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
42 STREET: 1251 Avenue of the Americas
43 CITY: New York
44 STATE: New York
45 COUNTRY: USA
46 ZIP: 10021
47
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: PC-DOS/MS-DOS
52 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/09/490,324
55 FILING DATE: 24-Jan-2000
56
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US/09/025,769
59 FILING DATE: 18-FEB-1998
60 APPLICATION NUMBER: EP 95 11 3021.0
61 FILING DATE: 18-AUG-1995
62
63 ATTORNEY/AGENT INFORMATION:
64 NAME: James F. Haley, Jr., Esq.
65 REGISTRATION NUMBER: 27,794
66 REFERENCE/DOCKET NUMBER: MORPHO/5
67 TELECOMMUNICATION INFORMATION:
68 TELEPHONE: (212)596-9000
69 TELEFAX: (212)596-9090
70
71 INFORMATION FOR SEQ ID NO: 36:
72 SEQUENCE CHARACTERISTICS:
73 LENGTH: 120 amino acids
74 TYPE: amino acid
75 STRANDEDNESS: <Unknown>
76 TOPOLOGY: linear
77 MOLECULE TYPE: protein
78 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
79
80

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US-09-490-324-36
Query Match      66.5%; Score 396.5; DB 4; Length 120;
Best Local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2

QY      1 VOLLEQSGAEVYKRPASVLTISCOASRODPFGQYIHWVQAPOQGFEMNGIINPSGGSANY 60
DB      2 VOLV-QSGAEVYKRPASVLTISCOASRODPFGQYIHWVQAPOQGFEMNGIINPSGGSANY 60
        1 APKPKGRGLTMRDSDTIVYMTLISLTSBDAIVVYCL-----LQALKHWGGCTLVAVSS 114
        61 AAKPKGRVTRDTSISTAYMELSLRSEDAIVVYCARMGDGFYAMDYWGCTLVAVSS 120

RESULT 8
US-09-490-324-59
Sequence 59, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-324-59

Query Match      66.5%; Score 396.5; DB 4; Length 120;
Best Local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2

QY      1 VOLLEQSGAEVYKRPASVLTISCOASRODPFGQYIHWVQAPOQGFEMNGIINPSGGSANY 60
DB      2 VOLV-QSGAEVYKRPASVLTISCOASRODPFGQYIHWVQAPOQGFEMNGIINPSGGSANY 60
        1 APKPKGRGLTMRDSDTIVYMTLISLTSBDAIVVYCL-----LQALKHWGGCTLVAVSS 114
        61 AAKPKGRVTRDTSISTAYMELSLRSEDAIVVYCARMGDGFYAMDYWGCTLVAVSS 120

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```

? Patent No. 6300064
? GENERAL INFORMATION:
? APPLICANT: Knappik, Achim
? APPLICANT: Pack, Peter
? APPLICANT: Ilag, Vic
? APPLICANT: Ge, Liming
? APPLICANT: Moroney, Simon
? APPLICANT: Plueckthun, Andreas
? TITLE OF INVENTION: Protein/(Poly)peptide libraries
? NUMBER OF SEQUENCES: 373
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
? STREET: 1251 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10021
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/025,769B
? FILING DATE: 18-FEB-1998
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: EP 95 11 3021.0
? FILING DATE: 18-AUG-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: James F. Haley, Jr., Esq.
? REGISTRATION NUMBER: 27,794
? REFERENCE/DOCKET NUMBER: MORPHO/5
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 596-9000
? TELEFAX: (212) 596-9090
? INFORMATION FOR SEQ ID NO: 22:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 117 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-025-769B-22
?
? Query Match 65.3%; Score 389; DB 3; Length 117;
? Best Local Similarity 64.1%; Pred. No. 1,1e-32;
? Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;
?
? QY 1 VOLIEGSGABYKRPGASVTTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPESGSANY 60
? |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
? Db 2 VOLV-OSGAELKKFGASVKKSCKASGYTFITSYWHWYRQAPGCGLEWNGWINPNSGNTNY 60
?
? QY 61 APEKKGILTMSRDSSTDTVYVMTLTSLSEDTAVVYVCLQ---ALKHMGCGTLVAVSS 114
? |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
? Db 61 AAKFGQSVTWTRDTYSISTAYMELSLKSDDTAVVYCARDDGCGFVWGGTLTVVSS 117
?
? RESULT 13
? US-09-490-070A-22
? Sequence 22, Application US/09490070A
? Patent No. 6696248
? GENERAL INFORMATION:
? APPLICANT: Knappik, Achim
? APPLICANT: Pack, Peter
? APPLICANT: Ilag, Vic
? APPLICANT: Ge, Liming
? APPLICANT: Moroney, Simon
? APPLICANT: Plueckthun, Andreas
? TITLE OF INVENTION: Protein/(Poly)peptide libraries
? NUMBER OF SEQUENCES: 373
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Colin G. SandercocK, Esq. c/o Heller Ehrman
? White & McCaulliffe
?

```

STREET: 1666 K Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-070A-22

Query Match 65.3%; Score 389; DB 4; Length 117;
Best Local Similarity 64.1%; Pred. No. 1.1e-32;
Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;

QY 1 VOLLEQSGAEVKRPGASVITISCOASRODFSGQYIHWRQAPGQGFEMWGIINSGGSANY 60
DB 2 VOLV-QSGAEVKRPGASVITISCOASRODFSGQYIHWRQAPGQGFEMWGIINSGGSANY 60

QY 61 APFKGRILMSRDSSTDTVYMTLTSLSDEPTAVYYCLQ--ALKHWGGTIVAVSS 114
DB 61 AQKFGRRVMTBTDISTAYMELSLRSDDTAVYYCARDDGGDFDWGGGTIVTVSS 117

RESULT 14
US-09-490-153-22
Sequence 22, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-153-22

Query Match 65.3%; Score 389; DB 4; Length 117;
Best Local Similarity 64.1%; Pred. No. 1.1e-32;
Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;

QY 1 VOLLEQSGAEVKRPGASVITISCOASRODFSGQYIHWRQAPGQGFEMWGIINSGGSANY 60
DB 2 VOLV-QSGAEVKRPGASVITISCOASRODFSGQYIHWRQAPGQGFEMWGIINSGGSANY 60

QY 61 APFKGRILMSRDSSTDTVYMTLTSLSDEPTAVYYCLQ--ALKHWGGTIVAVSS 114
DB 61 AQKFGRRVMTBTDISTAYMELSLRSDDTAVYYCARDDGGDFDWGGGTIVTVSS 117

RESULT 15
US-09-490-324-22
Sequence 22, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-324-22

Query Match      65.3%; Score 389; DB 4; Length 117;
Best Local Similarity 64.1%; Pred. No. 1.1e-32; Indels 4; Gaps 2;
Matches 75; Conservative 15; Mismatches 23;

QY 1 VQLLEQSGAEVKKRPGASVTISCOASRODPSGQYIHVYRQAPGQGFEMMGIIINPSGGSANY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VQLV-QSGAEVKKRPGASVVKSCASGYFTSYMHVYRQAPGQGLEFMGMGINPSGNTNY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 APKFKGRLLTMSRDSSTDTVTMTLTLTSEPTAVYYCLQ--ALKHMGQGLVAVSS 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGGRVWTTRDTSTAYMELSLRSDDTAVYYCARDGSGGFDYWGQGLVTVSS 117
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Search completed: November 9, 2005, 06:00:21
Job time: 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 05:52:18 ; Search time 166 Seconds
(without alignments)
265.607 Million cell updates/sec

Title: US-09-936-964A-36

Perfect score: 1 VQLLEQSGAEVKRPGASVTI.....YCLQLQKHWGQCTLVAVSS 114

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_16Dec04:*

1: geneeqp19808:*

2: geneeqp19908:*

3: geneeqp20008:*

4: geneeqp20018:*

5: geneeqp20028:*

6: geneeqp20038:*

7: geneeqp20048:*

8: geneeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 596 | 100.0 | 114 | 3 | AA18864 Amino aci |
| 2 | 596 | 100.0 | 114 | 3 | AA18860 Amino aci |
| 3 | 596 | 100.0 | 114 | 3 | AA18876 Amino aci |
| 4 | 596 | 100.0 | 114 | 3 | AA18862 Amino aci |
| 5 | 596 | 100.0 | 114 | 3 | AA18866 Amino aci |
| 6 | 590 | 99.0 | 114 | 3 | AA18868 Amino aci |
| 7 | 588 | 98.7 | 114 | 3 | AA18858 Amino aci |
| 8 | 578 | 97.0 | 114 | 3 | AA18874 Amino aci |
| 9 | 564 | 94.6 | 114 | 3 | AA18882 Amino aci |
| 10 | 536 | 89.9 | 114 | 3 | AA18880 Amino aci |
| 11 | 536 | 89.9 | 114 | 3 | AA18878 Amino aci |
| 12 | 536 | 89.9 | 114 | 3 | AA18870 Amino aci |
| 13 | 536 | 89.9 | 114 | 3 | AA18856 Amino aci |
| 14 | 536 | 89.9 | 114 | 3 | AA18872 Amino aci |
| 15 | 421 | 70.6 | 124 | 3 | AA18872 Amino aci |
| 16 | 419.5 | 70.4 | 124 | 3 | AA18872 Amino aci |
| 17 | 418 | 70.1 | 142 | 6 | AD447344 Human ant |
| 18 | 418 | 70.1 | 142 | 6 | AD447344 Human ant |
| 19 | 418 | 70.1 | 142 | 6 | AD447344 Human ant |
| 20 | 418 | 70.1 | 142 | 6 | AD447344 Human ant |
| 21 | 414 | 69.5 | 255 | 5 | AD447344 Human ant |
| 22 | 414 | 69.5 | 255 | 5 | AD447344 Human ant |
| 23 | 413.5 | 69.4 | 245 | 7 | AD447344 Human ant |
| 24 | 413.5 | 69.4 | 245 | 7 | AD447344 Human ant |
| 25 | 412 | 69.1 | 117 | 8 | AD447344 Human ant |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 412 | 69.1 | 117 | 8 | AD447344 Human ant |
| 27 | 412 | 69.1 | 249 | 8 | AD447344 Human ant |
| 28 | 412 | 69.1 | 249 | 8 | AD447344 Human ant |
| 29 | 411.5 | 69.0 | 241 | 7 | AD447344 Human ant |
| 30 | 410 | 68.8 | 248 | 5 | AD447344 Human ant |
| 31 | 410 | 68.8 | 248 | 5 | AD447344 Human ant |
| 32 | 409 | 68.6 | 248 | 5 | AD447344 Human ant |
| 33 | 409 | 68.6 | 248 | 5 | AD447344 Human ant |
| 34 | 408.5 | 68.5 | 125 | 5 | AD447344 Human ant |
| 35 | 408.5 | 68.5 | 249 | 5 | AD447344 Human ant |
| 36 | 408.5 | 68.5 | 249 | 5 | AD447344 Human ant |
| 37 | 408.5 | 68.5 | 249 | 5 | AD447344 Human ant |
| 38 | 408.5 | 68.5 | 249 | 5 | AD447344 Human ant |
| 39 | 408.5 | 68.5 | 251 | 5 | AD447344 Human ant |
| 40 | 408.5 | 68.5 | 251 | 5 | AD447344 Human ant |
| 41 | 408.5 | 68.5 | 254 | 5 | AD447344 Human ant |
| 42 | 408.5 | 68.5 | 254 | 5 | AD447344 Human ant |
| 43 | 407.5 | 68.4 | 114 | 7 | AD447344 Human ant |
| 44 | 407 | 68.3 | 258 | 5 | AD447344 Human ant |
| 45 | 407 | 68.3 | 258 | 5 | AD447344 Human ant |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | AA18864 standard; protein; 114 AA. |
| ID | AA18864 |
| AC | AA18864: |
| DT | 08-FEB-2001 (first entry) |
| DE | Amino acid sequence of anti-p53 antibody heavy chain clone 163.7. |
| XX | p53: antibody; immune response; vaccine; gene therapy; cancer; |
| KW | rheumatoid arthritis; coronary heart disease. |
| OS | Homo sapiens. |
| XX | WO2000056770-A1. |
| PN | 28-SEP-2000. |
| PD | 15-MAR-2000; 2000WO-AU000189. |
| XX | 19-MAR-1999; 99AU-00009321. |
| PR | (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD. |
| PA | Ward RL, Coomber DMU; |
| PI | WPI: 2000-638249/61. |
| XX | N-PSDB; AAA6141. |
| DR | Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide |
| XX | fragments, useful in treatment and diagnosis of cancer, rheumatoid |
| PT | arthritis and coronary heart disease. |
| XX | Claim 30; Page 139; 163pp; English. |
| XX | The present sequence represents the heavy chain of an antibody reactive |
| CC | against p53. The antibody is obtained from a vertebrate host expressing |
| CC | an immune response against a naturally occurring disease. The antibodies |
| CC | are useful in pharmaceutical compositions, which additionally contain |
| CC | chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes |
| CC | or gadolinium. The polypeptide components of the antibodies are useful in |
| CC | vaccines, for inducing an immune response against a disease in a |
| CC | vertebrate, for treatment and/or prophylaxis of disease and for detection |
| CC | purposes. The nucleic acid sequences can be used to detect a disease as |
| CC | well as for gene therapy and recombinant production of the polypeptides. |
| CC | In particular, the following can be treated cancer, rheumatoid arthritis |
| CC | and coronary heart disease. Cancers include carcinogenic tumours, tumours |

CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,1e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQLLEQSGAEVKRPGASVTISCOASRDPSGQYIHVWRQAPQGPFEMMGIIINPSGGSANY 60
Db 1 VQLLEQSGAEVKRPGASVTISCOASRDPSGQYIHVWRQAPQGPFEMMGIIINPSGGSANY 60

QY 61 APEFKGRLTMSRDSSTDYVMTLTSLTSEDTAVVYCLLQALHKGWGCTLVAVSS 114
Db 61 APEFKGRLTMSRDSSTDYVMTLTSLTSEDTAVVYCLLQALHKGWGCTLVAVSS 114

RESULT 2

AAB18860
ID AAB18860 standard; protein; 114 AA.

AC AAB18860;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.5.

KM p53; antibody; immune response; vaccine; gene therapy; cancer;

KM rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

PN MO200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000MO-AU000189.

PR 19-MAR-1999; 99AU-00009321.

PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

DR WPI; 2000-638249/61.

DR N-PSDB; AAA96137.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.

PS Claim 30; Page 135; 163pp; English.

XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,

CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,1e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQLLEQSGAEVKRPGASVTISCOASRDPSGQYIHVWRQAPQGPFEMMGIIINPSGGSANY 60
Db 1 VQLLEQSGAEVKRPGASVTISCOASRDPSGQYIHVWRQAPQGPFEMMGIIINPSGGSANY 60

QY 61 APEFKGRLTMSRDSSTDYVMTLTSLTSEDTAVVYCLLQALHKGWGCTLVAVSS 114
Db 61 APEFKGRLTMSRDSSTDYVMTLTSLTSEDTAVVYCLLQALHKGWGCTLVAVSS 114

RESULT 3

AAB18876
ID AAB18876 standard; protein; 114 AA.

AC AAB18876;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.20.

KM p53; antibody; immune response; vaccine; gene therapy; cancer;

KM rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

PN MO200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000MO-AU000189.

PR 19-MAR-1999; 99AU-00009321.

PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

DR WPI; 2000-638249/61.

DR N-PSDB; AAA96153.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.

PS Claim 30; Page 151; 163pp; English.

XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VOLLEQSGAEVYKRPQASVTISCOASRODPFSGQYIHWVROAPQGFEMWGIINPSCGSANY 60
DB 1 VOLLEQSGAEVYKRPQASVTISCOASRODPFSGQYIHWVROAPQGFEMWGIINPSCGSANY 60

QY 61 APKFKGRITMSRDSSTDTVYMTLSTLSEDTAVVYCCILQALKHMGQGLTAVVSS 114
DB 61 APKFKGRITMSRDSSTDTVYMTLSTLSEDTAVVYCCILQALKHMGQGLTAVVSS 114

RESULT 4
AAB18862
ID AAB18862 standard; protein; 114 AA.
XX
AC AAB18862;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.6.
XX
KM p53; antibody; immune response; vaccine; gene therapy; cancer;
KW rheumatoid arthritis; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200056770-A1.
XX
PD 28-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-AU000189.
XX
PR 19-MAR-1999; 99AU-00009321.
XX
PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
PI Ward RL, Coomber DMJ;
XX
DR WPI: 2000-638249/61.
DR N-PSDB; AAA96139.
XX

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX

PS Claim 30; Page 137; 163pp; English.

CC The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX

XX Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VOLLEQSGAEVYKRPQASVTISCOASRODPFSGQYIHWVROAPQGFEMWGIINPSCGSANY 60
DB 1 VOLLEQSGAEVYKRPQASVTISCOASRODPFSGQYIHWVROAPQGFEMWGIINPSCGSANY 60

QY 61 APKFKGRITMSRDSSTDTVYMTLSTLSEDTAVVYCCILQALKHMGQGLTAVVSS 114
DB 61 APKFKGRITMSRDSSTDTVYMTLSTLSEDTAVVYCCILQALKHMGQGLTAVVSS 114

RESULT 5
AAB18866
ID AAB18866 standard; protein; 114 AA.
XX
AC AAB18866;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.9.
XX
KM p53; antibody; immune response; vaccine; gene therapy; cancer;
KW rheumatoid arthritis; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200056770-A1.
XX
PD 28-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-AU000189.
XX
PR 19-MAR-1999; 99AU-00009321.
XX
PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
PI Ward RL, Coomber DMJ;
XX
DR WPI: 2000-638249/61.
DR N-PSDB; AAA96143.
XX

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX

PS Claim 30; Page 141; 163pp; English.

CC The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX

XX Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VOLLEQSGAEVYKRPQASVTISCOASRODPFSGQYIHWVROAPQGFEMWGIINPSCGSANY 60
DB 1 VOLLEQSGAEVYKRPQASVTISCOASRODPFSGQYIHWVROAPQGFEMWGIINPSCGSANY 60


```
XX AC AAB18874;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.17.
XX KM p53; antibody; immune response; vaccine; gene therapy; cancer;
XX KW rheumatoid arthritis; coronary heart disease.
XX OS Homo sapiens.
XX FT Key location/Qualifiers
XX FT Misc-difference 77 /note= "Glu encoded by GAC"
XX PN WO200056770-A1.
XX PD 28-SEP-2000.
XX PF 15-MAR-2000; 2000WO-AU000189.
XX PR 19-MAR-1999; 99AU-00009321.
XX PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX PI Ward RL, Coomber DMJ;
XX DR WPI; 2000-638249/61.
XX DR N-PSDB; AAA96151.
XX PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
XX PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
XX PT arthritis and coronary heart disease.
XX PS Claim 30; Page 149; 163pp; English.
XX CC The present sequence represents the heavy chain of an antibody reactive
XX CC against p53. The antibody is obtained from a vertebrate host expressing
XX CC an immune response against a naturally occurring disease. The antibodies
XX CC are useful in pharmaceutical compositions, which additionally contain
XX CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
XX CC or gadolinium. The polypeptide components of the antibodies are useful in
XX CC vaccines, for inducing an immune response against a disease in a
XX CC vertebrate, for treatment and/or prophylaxis of disease and for detection
XX CC purposes. The nucleic acid sequences can be used to detect a disease as
XX CC well as for gene therapy and recombinant production of the polypeptides.
XX CC In particular, the following can be treated cancer, rheumatoid arthritis
XX CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
XX CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
XX CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
XX CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
XX CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
XX CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX SQ Sequence 114 AA;
XX
XX Query Match 97.0%; Score 578; DB 3; Length 114;
XX Best Local Similarity 96.5%; Pred. No. 5e-45;
XX Matches 110; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 VOLLEOGGAEVKKRPGASVTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
DB 1 VOLLEOGGAEVKKRPGASVTISCRASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
QY 61 APRFKGLTMSRSDSTDTVYMTLTSLTSEDTAVYVYCLLQALKHWGQGTIVAVSS 114
DB 61 APRFKGLTMSRSDSTDTVYMTLTSLTSEDTAVYVYCLLQALKHWGQGTIVAVSS 114
XX
XX RESULT 9
XX AAB18882
XX ID AAB18882 standard; protein; 114 AA.
```

```
XX AC AAB18882;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.24.
XX KM p53; antibody; immune response; vaccine; gene therapy; cancer;
XX KW rheumatoid arthritis; coronary heart disease.
XX OS Homo sapiens.
XX FT Key location/Qualifiers
XX FT Misc-difference 77 /note= "Glu encoded by GAC"
XX PN WO200056770-A1.
XX PD 28-SEP-2000.
XX PF 15-MAR-2000; 2000WO-AU000189.
XX PR 19-MAR-1999; 99AU-00009321.
XX PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX PI Ward RL, Coomber DMJ;
XX DR WPI; 2000-638249/61.
XX DR N-PSDB; AAA96159.
XX PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
XX PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
XX PT arthritis and coronary heart disease.
XX PS Claim 30; Page 157; 163pp; English.
XX CC The present sequence represents the heavy chain of an antibody reactive
XX CC against p53. The antibody is obtained from a vertebrate host expressing
XX CC an immune response against a naturally occurring disease. The antibodies
XX CC are useful in pharmaceutical compositions, which additionally contain
XX CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
XX CC or gadolinium. The polypeptide components of the antibodies are useful in
XX CC vaccines, for inducing an immune response against a disease in a
XX CC vertebrate, for treatment and/or prophylaxis of disease and for detection
XX CC purposes. The nucleic acid sequences can be used to detect a disease as
XX CC well as for gene therapy and recombinant production of the polypeptides.
XX CC In particular, the following can be treated cancer, rheumatoid arthritis
XX CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
XX CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
XX CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
XX CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
XX CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
XX CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX SQ Sequence 114 AA;
XX
XX Query Match 94.6%; Score 564; DB 3; Length 114;
XX Best Local Similarity 93.0%; Pred. No. 9.5e-44;
XX Matches 106; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 VOLLEOGGAEVKKRPGASVTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
DB 1 VOLLEOGGAEVKKRPGASVTISCOASRONDFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
QY 61 APRFKGLTMSRSDSTDTVYMTLTSLTSEDTAVYVYCLLQALKHWGQGTIVAVSS 114
DB 61 APRFKGLTMSRSDSTDTVYMTLTSLTSEDTAVYVYCLLQALKHWGQGTIVAVSS 114
XX
XX RESULT 10
XX AAB18880
XX ID AAB18880 standard; protein; 114 AA.
```

```
XX Amino acid sequence of anti-p53 antibody heavy chain clone 163.23.
DE
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
KM rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
OS
XX MO200056770-A1.
PN
XX 28-SEP-2000.
PD
XX 15-MAR-2000; 2000MO-AU000189.
PF
XX 19-MAR-1999; 99AU-00009321.
PR
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
PA
XX Ward RL, Coomber DMJ;
PI
XX WPI: 2000-638249/61.
DR N-PSDB; AAA96157.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX
XX Claim 30; Page 155; 163pp; English.
PS
XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
CC
XX
XX Sequence 114 AA;
SQ
Query Match 89.9%; Score 536; DB 3; Length 114;
Best Local Similarity 88.6%; Pred. No. 3,4e-41;
Matches 101; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VQLEDSGAEVKRPASVTISCOASRDPSGQYIHWVROAPGQGFEMMGIIINSGGSANY 60
DB 1 VQLEDSGAEKMRPGASVTISCOASRDTFSGQYIHWVROAPGQGLEMGVINGSGGSANY 60
QY 61 APEFKGRLTMSRDSSTDTVYMTLTSLTSEDTAVYVYCLQALKHWGGTIVAASS 114
DB 61 APEFKGRLTMSRDSSTDTVYMTLTSLTSEDTAVYVYCLQALKHWGGTIVAASS 114
RESULT 11
AAB18878
ID AAB18878 standard; protein; 114 AA.
XX
XX AAB18878;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX Amino acid sequence of anti-p53 antibody heavy chain clone 163.22.
DE
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
KM
```

```
KM rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
OS
XX MO200056770-A1.
PN
XX 28-SEP-2000.
PD
XX 15-MAR-2000; 2000MO-AU000189.
PF
XX 19-MAR-1999; 99AU-00009321.
PR
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
PA
XX Ward RL, Coomber DMJ;
PI
XX WPI: 2000-638249/61.
DR N-PSDB; AAA96155.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX
XX Claim 30; Page 153; 163pp; English.
PS
XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
CC
XX
XX Sequence 114 AA;
SQ
Query Match 89.9%; Score 536; DB 3; Length 114;
Best Local Similarity 88.6%; Pred. No. 3,4e-41;
Matches 101; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VQLEDSGAEVKRPASVTISCOASRDPSGQYIHWVROAPGQGFEMMGIIINSGGSANY 60
DB 1 VQLEDSGAEKMRPGASVTISCOASRDTFSGQYIHWVROAPGQGLEMGVINGSGGSANY 60
QY 61 APEFKGRLTMSRDSSTDTVYMTLTSLTSEDTAVYVYCLQALKHWGGTIVAASS 114
DB 61 APEFKGRLTMSRDSSTDTVYMTLTSLTSEDTAVYVYCLQALKHWGGTIVAASS 114
RESULT 12
AAB18870
ID AAB18870 standard; protein; 114 AA.
XX
XX AAB18870;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX Amino acid sequence of anti-p53 antibody heavy chain clone 163.15.
DE
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
KM rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
OS
```

PN WO200056770-A1.
XX 28-SEP-2000.
XX
XX
PF 15-MAR-2000; 2000WO-AU000189.
XX
XX 19-MAR-1999; 99AU-00009321.
XX
PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX WPI: 2000-638249/61.
DR N-PSDB; AAA96147.
XX
PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX
PS Claim 30; Page 145; 163pp; English.
XX
XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX
SQ Sequence 114 AA;
XX
Query Match 89.9%; Score 536; DB 3; Length 114;
Best Local Similarity 88.6%; Pred. No. 3.4e-41;
Matches 101; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VOLLESGAEVKRPGASVTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
DB 1 VOLLESGAEVKRPGASVTISCOASROTFSGQYIHWYRQAPGCGLEMMGVINPSGGSANY 60
QY 61 APRFKGRLTMSRSDSTDTVTMTLTSLTSEDTAVYYCLQALKHWGQGLTVAVSS 114
DB 61 APFQGLTMSRSDASTVTYMKLSLTSEDTAVYYCLQALKYWGQGLTVAVSS 114
RESULT 13
AAB18856
ID AAB18856 standard; protein; 114 AA.
XX
XX AAB18856;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.1.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
KM rheumatoid arthritis; coronary heart disease.
XX
OS Homo sapiens.
XX
XX WO200056770-A1.
XX
XX PD 28-SEP-2000.
XX

PF 15-MAR-2000; 2000WO-AU000189.
XX
XX 19-MAR-1999; 99AU-00009321.
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX WPI: 2000-638249/61.
DR N-PSDB; AAA96133.
XX
PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX
PS Claim 30; Page 131; 163pp; English.
XX
XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX
SQ Sequence 114 AA;
XX
Query Match 89.9%; Score 536; DB 3; Length 114;
Best Local Similarity 88.6%; Pred. No. 3.4e-41;
Matches 101; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VOLLESGAEVKRPGASVTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
DB 1 VOLLESGAEVKRPGASVTISCOASROTFSGQYIHWYRQAPGCGLEMMGVINPSGGSANY 60
QY 61 APRFKGRLTMSRSDSTDTVTMTLTSLTSEDTAVYYCLQALKHWGQGLTVAVSS 114
DB 61 APFQGLTMSRSDASTVTYMKLSLTSEDTAVYYCLQALKYWGQGLTVAVSS 114
RESULT 14
AAB18872
ID AAB18872 standard; protein; 114 AA.
XX
XX AAB18872;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.16.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
KM rheumatoid arthritis; coronary heart disease.
XX
OS Homo sapiens.
XX
XX WO200056770-A1.
XX
XX PD 28-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-AU000189.
XX
XX PR 19-MAR-1999; 99AU-00009321.
XX

PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX
XX WPI; 2000-638249/61.
XX
XX N-PSDB; AAA96149.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease.
XX
XX
XX Claim 30; Page 147; 163pp; English.
XX
XX The present sequence represents the heavy chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma
XX
XX Sequence 114 AA;
SQ
Query Match 89.9%; Score 536; DB 3; Length 114;
Best Local Similarity 88.6%; Pred. No. 3,4e-41;
Matches 101; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VOLLESGAEVKKRPGASVTITSCQASRODFSGOYIHWVROAPGOGFEMWGIINSGGSANY 60
DB 1 VOLLESGAEMKRPASVITSCQASRQTFSGOYIHWVROAPGOGLEMMGIINSGGSANY 60
QY 61 APKFKGRLTMSRDSSTDTVTYMTLTSLTSEDTAVYYCCLQALKHWGQGLTVAVSS 114
DB 61 APFGQRLTMSRDSSTDTVTYMTLTSLTSEDTAVYYCCLQALKHWGQGLTVAVSS 114
Db 61 APFGQRLTMSRDSSTDTVTYMTLTSLTSEDTAVYYCCLQALKHWGQGLTVAVSS 114
RESULT 15
AAV15127
ID AAV15127 standard; protein: 242 AA.
XX
XX AAV15127;
AC
XX
XX 07-FEB-2000 (first entry)
DT
XX
XX Anti-murine CTLA-4 M19 sFV.
DE
XX
XX Anti-murine CTLA-4 sFV; M19 sFV; single chain antibody; murine CTLA4;
KM membrane-associated protein; chimeric construct; extracellular domain;
KM human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
KM recipient CD28; T-cell proliferation;
KM xenograft-specific immunosuppression.
XX
XX Mus gp.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 208
FT /note= "Corresponds to atc codon"
XX
XX WO9557266-A2.
XX
XX 11-NOV-1999.
XX

PF 30-APR-1999; 99WO-GB001350.
XX
XX 30-APR-1998; 98GB-00009280.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Lechler IR, Dorling A;
XX
XX WPI; 2000-038415/03.
XX
XX N-PSDB; AA228999.
XX
XX Inhibiting T-cell mediated rejection of xenotransplanted organs.
XX
XX
XX Claim 9; Fig 11; 43pp; English.
XX
XX The present sequence is the anti-murine CTLA-4 sFV (M19 sFV). This is a
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
CC comprising DNA sequences encoding the extracellular domain of murine
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFV protein.
CC The anti-hCTLA4 sFV functions as a ligand binding to CTLA-4 on activated
CC T-cells and antagonises the co-stimulatory signal provided by the
CC interaction between donor B7 and recipient CD28. Cells expressing the
CC anti-hCTLA4 sFV failed to stimulate T-cell proliferation. This is used in
CC xenograft-specific immunosuppression
XX
XX Sequence 242 AA;
SQ
Query Match 70.6%; Score 421; DB 3; Length 242;
Best Local Similarity 69.7%; Pred. No. 2,2e-30;
Matches 83; Conservative 12; Mismatches 18; Indels 6; Gaps 2;
QY 1 VOLLESGAEVKKRPGASVTITSCQASRODFSGOYIHWVROAPGOGFEMWGIINSGGSANY 60
DB 2 VOLV-QSGAEVKKRPGASVSVCKASGYTFTSYIMHWROAPGOGLEMMGIINSGGSTSY 60
QY 61 APKFKGRLTMSRDSSTDTVTYMTLTSLTSEDTAVYYC----LQALKHWGQGLTVAVSS 114
DB 61 AQKFGQRYVTMTBDTSTSTYVMEISLRSSEDTAVYYCARVAPVYNTLVFWGQGLTVAVSS 119
Db 61 AQKFGQRYVTMTBDTSTSTYVMEISLRSSEDTAVYYCARVAPVYNTLVFWGQGLTVAVSS 119
Search completed: November 9, 2005, 05:59:09
Job time : 168 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 05:52:17 : Search time 165 Seconds

(without alignments)
289.083 Million cell updates/sec

Title: US-09-936-964A-36

Perfect score: 1 VQLLEQSGAEVKRGASVTI.....YCLLQALKHMGCTLVAVSS 114

Sequence: 1 VQLLEQSGAEVKRGASVTI.....YCLLQALKHMGCTLVAVSS 114

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*

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12: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*

13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep.*

18: /cgn2_6/ptodata/1/pubppaa/US10F_PUBCOMB.pep.*

19: /cgn2_6/ptodata/1/pubppaa/US10G_PUBCOMB.pep.*

20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 418 | 70.1 | 142 | 14 | US-10-171-452A-2 |
| 2 | 418 | 70.1 | 142 | 15 | US-10-353-708-2 |
| 3 | 418 | 70.1 | 142 | 16 | US-10-731-984-36 |
| 4 | 414 | 69.5 | 255 | 10 | US-09-880-748-1156 |
| 5 | 414 | 69.5 | 255 | 15 | US-10-293-418-1156 |
| 6 | 413.5 | 69.4 | 245 | 10 | US-09-880-748-1156 |
| 7 | 413.5 | 69.4 | 245 | 15 | US-10-293-418-1156 |
| 8 | 412 | 69.1 | 117 | 16 | US-10-688-925-16 |
| 9 | 412 | 69.1 | 249 | 16 | US-10-688-925-14 |
| 10 | 412 | 69.1 | 249 | 16 | US-10-688-925-14 |
| 11 | 412 | 69.1 | 249 | 16 | US-10-688-925-26 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 12 | 411.5 | 69.0 | 241 | 17 | US-10-935-290-72 | Sequence 72, Appl |
| 13 | 410 | 68.8 | 248 | 10 | US-09-880-748-2091 | Sequence 2091, Ap |
| 14 | 410 | 68.8 | 248 | 15 | US-10-293-418-2091 | Sequence 2091, Ap |
| 15 | 409 | 68.6 | 248 | 10 | US-09-880-748-1178 | Sequence 1178, Ap |
| 16 | 409 | 68.6 | 248 | 15 | US-10-293-418-1178 | Sequence 1178, Ap |
| 17 | 408.5 | 68.5 | 125 | 16 | US-10-466-242-13 | Sequence 13, Appl |
| 18 | 408.5 | 68.5 | 249 | 10 | US-09-880-748-1290 | Sequence 1290, Ap |
| 19 | 408.5 | 68.5 | 249 | 10 | US-09-880-748-1290 | Sequence 1290, Ap |
| 20 | 408.5 | 68.5 | 249 | 15 | US-10-293-418-1290 | Sequence 1290, Ap |
| 21 | 408.5 | 68.5 | 249 | 15 | US-10-293-418-1290 | Sequence 1290, Ap |
| 22 | 408.5 | 68.5 | 251 | 10 | US-09-880-748-1459 | Sequence 1459, Ap |
| 23 | 408.5 | 68.5 | 251 | 15 | US-10-293-418-1459 | Sequence 1459, Ap |
| 24 | 408.5 | 68.5 | 254 | 10 | US-09-880-748-1983 | Sequence 1983, Ap |
| 25 | 406.5 | 68.5 | 254 | 15 | US-10-293-418-1983 | Sequence 1983, Ap |
| 26 | 407 | 68.3 | 258 | 10 | US-09-880-748-2090 | Sequence 2090, Ap |
| 27 | 407 | 68.3 | 258 | 15 | US-10-293-418-2090 | Sequence 2090, Ap |
| 28 | 406 | 68.1 | 118 | 16 | US-10-466-242-29 | Sequence 29, Appl |
| 29 | 403.5 | 67.7 | 243 | 10 | US-09-880-748-1947 | Sequence 1947, Ap |
| 30 | 403.5 | 67.7 | 243 | 15 | US-10-293-418-1947 | Sequence 1947, Ap |
| 31 | 403.5 | 67.7 | 254 | 10 | US-09-880-748-1961 | Sequence 1961, Ap |
| 32 | 403.5 | 67.7 | 254 | 15 | US-10-293-418-1961 | Sequence 1961, Ap |
| 33 | 402.5 | 67.5 | 114 | 15 | US-10-309-762-141 | Sequence 141, App |
| 34 | 402 | 67.4 | 253 | 10 | US-09-880-748-1359 | Sequence 1359, Ap |
| 35 | 402 | 67.4 | 253 | 15 | US-10-293-418-1359 | Sequence 1359, Ap |
| 36 | 401 | 67.3 | 123 | 20 | US-11-039-767-14 | Sequence 14, Appl |
| 37 | 399.5 | 67.0 | 245 | 18 | US-10-943-197-5 | Sequence 5, Appl1 |
| 38 | 399 | 66.9 | 247 | 10 | US-09-880-748-1899 | Sequence 1899, Ap |
| 39 | 399 | 66.9 | 247 | 15 | US-10-293-418-1899 | Sequence 1899, Ap |
| 40 | 399 | 66.9 | 248 | 10 | US-09-880-748-959 | Sequence 959, App |
| 41 | 399 | 66.9 | 248 | 15 | US-10-293-418-959 | Sequence 959, App |
| 42 | 399 | 66.9 | 256 | 10 | US-09-880-748-1967 | Sequence 1967, Ap |
| 43 | 399 | 66.9 | 256 | 15 | US-10-293-418-1967 | Sequence 1967, Ap |
| 44 | 398.5 | 66.9 | 132 | 9 | US-09-811-737-10 | Sequence 10, Appl |
| 45 | 398.5 | 66.9 | 260 | 9 | US-09-811-737-16 | Sequence 16, Appl |

RESULT 1

US-10-171-452A-2

Sequence 2, Appl1

Publication NO. US20030108518A1

GENERAL INFORMATION:

APPLICANT: Frewin, Mark

APPLICANT: Waldmann, Herman

APPLICANT: Gorman, Scott

APPLICANT: Hale, Geoff

APPLICANT: Rao, Patricia

APPLICANT: Kornaga, Tadeusz

APPLICANT: Ringler, Douglas

APPLICANT: Cobbold, Stephen

APPLICANT: Winsor-Hines, Dawn

TITLE OF INVENTION: TRX1 Antibody and Uses Therefor

FILE REFERENCE: 695458-59

CURRENT APPLICATION NUMBER: US/10/171,452A

PRIOR FILING DATE: 2003-02-10

PRIOR APPLICATION NUMBER: US60/373,471

PRIOR FILING DATE: 2002-04-18

PRIOR APPLICATION NUMBER: US60/373,470

PRIOR FILING DATE: 2002-04-18

PRIOR APPLICATION NUMBER: US60/345,194

PRIOR FILING DATE: 2002-10-19

PRIOR APPLICATION NUMBER: GB0122724.8

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: GB0114517.6

PRIOR FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 2

LENGTH: 142

TYPE: PRT

ORGANISM: Homo sapiens

US-10-171-452A-2

Query Match 70.1%; Score 418; DB 14; Length 142;
Best Local Similarity 63.8%; Pred. No. 2.7e-31;
Matches 81; Conservative 15; Mismatches 17; Indels 14; Gaps 2;

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QY 1 VOLLESGAEVKKPGASVTTISQASRQDFSGQYIHWVROAPGQGFEMWGIINPSGSANY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 12 VOLV-QSGAEVKKPGASVKKSCASGYTFNNYMHVROAPGQGLEWGIINPSGNSY 70
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APEKGRILMSRSSSDTYVMITLSLTSEPTAVYYC-----LLQALKHMGOG 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 71 AOKFGQGVMTTRDTSTSTVYMELSLRSEDTAVYYCAREKLTATTFGVLIITGMIDYWGOG 130
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 108 TLVAVSS 114
    |||:|||||
Db 131 TLVTVSS 137
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RESULT 2

US-10-353-708-2
; Sequence 2, Application US/10353708
; Publication No. US20030219403A1

; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-353-708-2

Query Match 70.1%; Score 418; DB 15; Length 142;
Best Local Similarity 63.8%; Pred. No. 2.7e-31;
Matches 81; Conservative 15; Mismatches 17; Indels 14; Gaps 2;

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QY 1 VOLLESGAEVKKPGASVTTISQASRQDFSGQYIHWVROAPGQGFEMWGIINPSGSANY 60
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Db 12 VOLV-QSGAEVKKPGASVKKSCASGYTFNNYMHVROAPGQGLEWGIINPSGNSY 70
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APEKGRILMSRSSSDTYVMITLSLTSEPTAVYYC-----LLQALKHMGOG 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 71 AOKFGQGVMTTRDTSTSTVYMELSLRSEDTAVYYCAREKLTATTFGVLIITGMIDYWGOG 130
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 108 TLVAVSS 114
    |||:|||||
Db 131 TLVTVSS 137
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RESULT 3

US-10-731-984-36
; Sequence 36, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: T1N-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; PRIOR FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-731-984-36

Query Match 70.1%; Score 418; DB 16; Length 142;
Best Local Similarity 63.8%; Pred. No. 2.7e-31;
Matches 81; Conservative 15; Mismatches 17; Indels 14; Gaps 2;

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QY 1 VOLLESGAEVKKPGASVTTISQASRQDFSGQYIHWVROAPGQGFEMWGIINPSGSANY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 12 VOLV-QSGAEVKKPGASVKKSCASGYTFNNYMHVROAPGQGLEWGIINPSGNSY 70
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APEKGRILMSRSSSDTYVMITLSLTSEPTAVYYC-----LLQALKHMGOG 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 71 AOKFGQGVMTTRDTSTSTVYMELSLRSEDTAVYYCAREKLTATTFGVLIITGMIDYWGOG 130
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 108 TLVAVSS 114
    |||:|||||
Db 131 TLVTVSS 137
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RESULT 4
US-09-880-748-1156
; Sequence 1156, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1156
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1156

Query Match 69.5%; Score 414; DB 10; Length 255;
Best Local Similarity 63.2%; Pred. No. 1.2e-30;
Matches 79; Conservative 14; Mismatches 18; Indels 14; Gaps 1;

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      4  FKGLTMSRDSSTDTVTMTLTSLTSEPTAVYYC-----LQALKHWGGTL 109
Qy      64  FKGLTMSRDSSTDTVTMTLTSLTSEPTAVYYC-----LQALKHWGGTL 109
      64  FQGVVTMTTRDTSTVTVMELSLRSEPTAVYYCARGGSEYDILGTGYGLGVYDVGQGT 123
Db      110  VAVSS 114
      124  VTAVSS 128
      124  VTAVSS 128

RESULT 5
US-10-293-418-1156
; Sequence 1156, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1156
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1156

Query Match      69.5%; Score 414; DB 15; Length 255;
Best Local Similarity 63.2%; Pred. No. 1.2e-30;
Matches 79; Conservative 14; Mismatches 18; Indels 14; Gaps 1;

Qy      4  LEQSGAEVKKRPGASVTKSCASRODFSGQYIHWWRQAPGQGFEMWGIINPSGGSANYAPK 63
      4  LQSGAEVKKRPGASVTKSCASGTYFTSYHWRQAPGQGLEWMGIINPSGGSSTYAK 63
Db      4  LQSGAEVKKRPGASVTKSCASGTYFTSYHWRQAPGQGLEWMGIINPSGGSSTYAK 63
Qy      64  FKGLTMSRDSSTDTVTMTLTSLTSEPTAVYYC-----LQALKHWGGTL 109
      64  FQGVVTMTTRDTSTVTVMELSLRSEPTAVYYCARGGSEYDILGTGYGLGVYDVGQGT 123
Db      110  VAVSS 114
      124  VTAVSS 128

RESULT 6
US-09-880-748-1919
; Sequence 1919, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
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      PRIOR FILING DATE: 2000-06-15
      PRIOR APPLICATION NUMBER: 60/240,816
      PRIOR FILING DATE: 2000-10-17
      PRIOR APPLICATION NUMBER: 60/276,248
      PRIOR FILING DATE: 2001-03-16
      PRIOR APPLICATION NUMBER: 60/277,379
      PRIOR FILING DATE: 2001-03-21
      PRIOR APPLICATION NUMBER: 60/293,499
      PRIOR FILING DATE: 2001-05-25
      NUMBER OF SEQ ID NOS: 3239
      SOFTWARE: PatentIn Ver. 2.0
      SEQ ID NO 1919
      LENGTH: 245
      TYPE: PRT
      ORGANISM: Homo sapiens
US-09-880-748-1919

Query Match      69.4%; Score 413.5; DB 10; Length 245;
Best Local Similarity 66.4%; Pred. No. 1.2e-30;
Matches 81; Conservative 14; Mismatches 18; Indels 9; Gaps 2;

Qy      1  VOLLEQSGAEVKKRPGASVTKSCASRODFSGQYIHWWRQAPGQGFEMWGIINPSGGSANY 60
      2  VOLV-QSGAEVKKRPGASVTKSCASGTYFTSYHWRQAPGQGLEWMGIINPSGGSSTY 60
Db      61  APFKGRLTMSRDSSTDTVTMTLTSLTSEPTAVYYC-----LQALKHWGGTLVAV 112
      61  AOKFQGVVTMTTRDTSTVTVMELSLRSEPTAVYYCARDLGSGYFSRYPDYWGQGLTVT 120
Qy      113  SS 114
      121  SS 122

RESULT 7
US-10-293-418-1919
; Sequence 1919, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1919
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1919

Query Match      69.4%; Score 413.5; DB 15; Length 245;
Best Local Similarity 66.4%; Pred. No. 1.2e-30;
Matches 81; Conservative 14; Mismatches 18; Indels 9; Gaps 2;

Qy      1  VOLLEQSGAEVKKRPGASVTKSCASRODFSGQYIHWWRQAPGQGFEMWGIINPSGGSANY 60
      1  VOLLEQSGAEVKKRPGASVTKSCASRODFSGQYIHWWRQAPGQGFEMWGIINPSGGSANY 60
```

```
Db      2 VOLV-QSGAEVKKPGASVKASCAGYFTSYMHVWRQAPQGQLEWMGIINPSSGSTSY 60
QY      61 APFKGRLTMSRSSSTDVYMTLTSLTSEPTAVYYC-----LLOALKHMGQTLVAVS 112
Db      61 AOKFQGRVTMTSDTSTSTVYMWELSLRSEDTAVYYCARDLGSYSFRRYPDWQGTLLVTV 120
QY      113 SS 114
Db      121 SS 122

RESULT 8
US-10-688-925-16
; Sequence 16, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertnuida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688,925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-16

Query Match      69.1%; Score 412; DB 16; Length 117;
Best Local Similarity 69.2%; Pred. No. 8e-31;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

QY      1 VOLLEQSGAEVKKPGASVTTISQASRQDPSGQYIHVWRQAPQGQFEMWGIINPSSGSANY 60
Db      2 VOLV-QSGAEVKKPGASVKASCAGYFTSYMHVWRQAPQGQLEWMGIINPSSGSTSY 60
QY      61 APFKGRLTMSRSSSTDVYMTLTSLTSEPTAVYYCCLQ--ALKHMGQTLVAVS 114
Db      61 AOKFQGRVTMTSDTSTSTVYMWELSLRSEDTAVYYCARDENMGFPDWQGTLLVTVSS 117

RESULT 9
US-10-688-925-28
; Sequence 28, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertnuida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688,925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-28

Query Match      69.1%; Score 412; DB 16; Length 117;
Best Local Similarity 69.2%; Pred. No. 8e-31;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

QY      1 VOLLEQSGAEVKKPGASVTTISQASRQDPSGQYIHVWRQAPQGQFEMWGIINPSSGSANY 60
Db      2 VOLV-QSGAEVKKPGASVKASCAGYFTSYMHVWRQAPQGQLEWMGIINPSSGSTSY 60
QY      61 APFKGRLTMSRSSSTDVYMTLTSLTSEPTAVYYCCLQ--ALKHMGQTLVAVS 114
Db      61 AOKFQGRVTMTSDTSTSTVYMWELSLRSEDTAVYYCARDENMGFPDWQGTLLVTVSS 117
```

```
RESULT 10
US-10-688-925-14
; Sequence 14, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertnuida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688,925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-14

Query Match      69.1%; Score 412; DB 16; Length 249;
Best Local Similarity 69.2%; Pred. No. 1.7e-30;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

QY      1 VOLLEQSGAEVKKPGASVTTISQASRQDPSGQYIHVWRQAPQGQFEMWGIINPSSGSANY 60
Db      2 VOLV-QSGAEVKKPGASVKASCAGYFTSYMHVWRQAPQGQLEWMGIINPSSGSTSY 60
QY      61 APFKGRLTMSRSSSTDVYMTLTSLTSEPTAVYYCCLQ--ALKHMGQTLVAVS 114
Db      61 AOKFQGRVTMTSDTSTSTVYMWELSLRSEDTAVYYCARDENMGFPDWQGTLLVTVSS 117

RESULT 11
US-10-688-925-26
; Sequence 26, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertnuida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688,925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-26

Query Match      69.1%; Score 412; DB 16; Length 249;
Best Local Similarity 69.2%; Pred. No. 1.7e-30;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

QY      1 VOLLEQSGAEVKKPGASVTTISQASRQDPSGQYIHVWRQAPQGQFEMWGIINPSSGSANY 60
Db      2 VOLV-QSGAEVKKPGASVKASCAGYFTSYMHVWRQAPQGQLEWMGIINPSSGSTSY 60
QY      61 APFKGRLTMSRSSSTDVYMTLTSLTSEPTAVYYCCLQ--ALKHMGQTLVAVS 114
Db      61 AOKFQGRVTMTSDTSTSTVYMWELSLRSEDTAVYYCARDENMGFPDWQGTLLVTVSS 117

RESULT 12
US-10-935-290-72
; Sequence 72, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GNAH
; FILE REFERENCE: PFS64P1
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
```



```
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/366,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 72
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scfv protein GMBG46
US-10-935-290-72
```

```
Query Match          69.0%; Score 411.5; DB 17; Length 241;
Best Local Similarity 66.9%; Pred. No. 1.9e-30;
Matches 79; Conservative 17; Mismatches 17; Indels 5; Gaps 2;
```

```
QY 1 VOLLEQSGAEVKKRPGASVTTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLV-QSGAEVKKRPGASVKKSCASGTYFTSYIHWYRQAPGCGLEMMGIINPSGGSITSY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APEKRGRLTMSRDSSTDTVTMTLTSLTSEDTAVYCC---LLOALKIMGGCTLVAVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGQGVMTWTRDTSTSTVWELSLRSEDTAVMYCARERFLRGMQDVWGRGTWTVVSS 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 13

```
US-09-880-748-2091
; Sequence 2091, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2091
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2091
```

```
Query Match          68.8%; Score 410; DB 10; Length 248;
Best Local Similarity 65.3%; Pred. No. 2.7e-30;
Matches 79; Conservative 17; Mismatches 17; Indels 8; Gaps 2;
```

```
QY 1 VOLLEQSGAEVKKRPGASVTTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLV-QSGAEVKKRPGASVKKSCASGTYFTSYIHWYRQAPGCGLEMMGIINPSGGSITSY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APEKRGRLTMSRDSSTDTVTMTLTSLTSEDTAVYCCLOALK-----HWGGCTLVAVS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGQGVMTWTRDTSTSTVWELSLRSEDTAVYFCARSTLEVATDQFDYWGQGTWTVSS 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 114 S 114
Db 121 S 121
```

```
RESULT 14
US-10-293-418-2091
; Sequence 2091, Application US/102993418
```

```
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2091
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2091
```

```
Query Match          68.8%; Score 410; DB 15; Length 248;
Best Local Similarity 65.3%; Pred. No. 2.7e-30;
Matches 79; Conservative 17; Mismatches 17; Indels 8; Gaps 2;
```

```
QY 1 VOLLEQSGAEVKKRPGASVTTISCOASRODFSGQYIHWYRQAPGCGFEMWGIINPSGGSANY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VOLV-QSGAEVKKRPGASVKKSCASGTYFTSYIHWYRQAPGCGLEMMGIINPSGGSITSY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APEKRGRLTMSRDSSTDTVTMTLTSLTSEDTAVYCCLOALK-----HWGGCTLVAVS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGQGVMTWTRDTSTSTVWELSLRSEDTAVYFCARSTLEVATDQFDYWGQGTWTVSS 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 114 S 114
Db 121 S 121
```

RESULT 15

```
US-09-880-748-1178
; Sequence 1178, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1178
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-880-748-1178

| | | | | |
|-----------------------|--------|-------------------|--------|-------------|
| Query Match | 68.6%; | Score 409; | DB 10; | Length 248; |
| Best Local Similarity | 64.9%; | Prod No. 3 30-20; | | |

Best Local Similarity 64.8%; Pred. No. 3.3e-30;

Matches 81; Conservative 14; Mismatches 18; Indels 12; Gaps 2;

OY 1 VQLLEQSGAEVKKRPGASVTISCSQASRDPSGGQIHWHTQAPRGGCFEMMGIINPSCGSANY 60
||| : ||||| : ||| : : ||||| : ||||| :
Dd 2 VQLV-QSGAEVKKPGASVKSCKASGYTFTSYVMHWTRQAPRGGLMMGIINPSCGSTSY 60

2 VQLV-QSGAEVKKPGASVKVSCASGYFTSYMHMVRQAPGQGLEWMGIINPSGGSY 60

Dy 61 A P K K G R L M S R D S T D Y V M T I T S L T S E D T A V Y C L ----- L Q A L K H W G O G T L 109
 | :
Db 61 A Q K G R V M T R D T S T S T V Y M E L S L R S E D T A V Y Y C A R E H Y D I L T G Y S L L G M D W M G R T L 120

61 A Q K F G R V T M R D T S T V M E L S L R S E D T A V Y C A R E H Y D I L T G Y S L L G M D V M G R G T L 120

QY 110 VAVSS 114

Db 1.21 VTSS 125

Search completed: November 9, 2005, 05:55:11
Job time : 166 secs

Job time : 166 secs